

SEQUENCE LISTING

<110> Maxygen ApS; Maxygen Holdings

<120> FVII or FVIIa variants having increased clotting activity

<130> 0267wo310

<140>

<141>

<160> 34

<170> PatentIn Ver. 2.1

<210> 1

<211> 406

<212> PRT

<213> Homo sapiens

<400> 1

Ala	Asn	Ala	Phe	Leu	Glu	Glu	Leu	Arg	Pro	Gly	Ser	Leu	Glu	Arg	Glu
1				5					10					15	
Cys	Lys	Glu	Glu	Gln	Cys	Ser	Phe	Glu	Glu	Ala	Arg	Glu	Ile	Phe	Lys
		20						25					30		
Asp	Ala	Glu	Arg	Thr	Lys	Leu	Phe	Trp	Ile	Ser	Tyr	Ser	Asp	Gly	Asp
		35					40					45			
Gln	Cys	Ala	Ser	Ser	Pro	Cys	Gln	Asn	Gly	Gly	Ser	Cys	Lys	Asp	Gln
	50					55					60				
Leu	Gln	Ser	Tyr	Ile	Cys	Phe	Cys	Leu	Pro	Ala	Phe	Glu	Gly	Arg	Asn
	65				70					75					80
Cys	Glu	Thr	His	Lys	Asp	Asp	Gln	Leu	Ile	Cys	Val	Asn	Glu	Asn	Gly
				85					90					95	
Gly	Cys	Glu	Gln	Tyr	Cys	Ser	Asp	His	Thr	Gly	Thr	Lys	Arg	Ser	Cys
			100					105					110		
Arg	Cys	His	Glu	Gly	Tyr	Ser	Leu	Leu	Ala	Asp	Gly	Val	Ser	Cys	Thr
		115					120					125			
Pro	Thr	Val	Glu	Tyr	Pro	Cys	Gly	Lys	Ile	Pro	Ile	Leu	Glu	Lys	Arg
	130					135					140				
Asn	Ala	Ser	Lys	Pro	Gln	Gly	Arg	Ile	Val	Gly	Gly	Lys	Val	Cys	Pro
	145				150					155					160
Lys	Gly	Glu	Cys	Pro	Trp	Gln	Val	Leu	Leu	Val	Asn	Gly	Ala	Gln	
			165					170					175		
Leu	Cys	Gly	Gly	Thr	Leu	Ile	Asn	Thr	Ile	Trp	Val	Val	Ser	Ala	Ala
			180				185						190		
His	Cys	Phe	Asp	Lys	Ile	Lys	Asn	Trp	Arg	Asn	Leu	Ile	Ala	Val	Leu
		195					200				205				
Gly	Glu	His	Asp	Leu	Ser	Glu	His	Asp	Gly	Asp	Glu	Gln	Ser	Arg	Arg
	210					215					220				
Val	Ala	Gln	Val	Ile	Ile	Pro	Ser	Thr	Tyr	Val	Pro	Gly	Thr	Thr	Asn
	225				230					235					240
His	Asp	Ile	Ala	Leu	Leu	Arg	Leu	His	Gln	Pro	Val	Val	Leu	Thr	Asp
			245					250					255		
His	Val	Val	Pro	Leu	Cys	Leu	Pro	Glu	Arg	Thr	Phe	Ser	Glu	Arg	Thr
			260					265					270		
Leu	Ala	Phe	Val	Arg	Phe	Ser	Leu	Val	Ser	Gly	Trp	Gly	Gln	Leu	Leu
	275					280						285			
Asp	Arg	Gly	Ala	Thr	Ala	Leu	Glu	Leu	Met	Val	Leu	Asn	Val	Pro	Arg
	290				295					300					
Leu	Met	Thr	Gln	Asp	Cys	Leu	Gln	Gln	Ser	Arg	Lys	Val	Gly	Asp	Ser
	305				310					315					320

Pro	Asn	Ile	Thr	Glu	Tyr	Met	Phe	Cys	Ala	Gly	Tyr	Ser	Asp	Gly	Ser
				325					330					335	
Lys	Asp	Ser	Cys	Lys	Gly	Asp	Ser	Gly	Gly	Pro	His	Ala	Thr	His	Tyr
			340					345					350		
Arg	Gly	Thr	Trp	Tyr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Gln	Gly	Cys
		355					360					365			
Ala	Thr	Val	Gly	His	Phe	Gly	Val	Tyr	Thr	Arg	Val	Ser	Gln	Tyr	Ile
		370				375					380				
Glu	Trp	Leu	Gln	Lys	Leu	Met	Arg	Ser	Glu	Pro	Arg	Pro	Gly	Val	Leu
385					390					395					400
Leu	Arg	Ala	Pro	Phe	Pro										
				405											

<210> 2

<211> 1338

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115)..(1335)

<400> 2

atgggtcagcc aggcctccg cctcctgtgc ctgctcctgg ggctgcaggg ctgcctggct 60

gccgtcttcg tcaccagga ggaagcccat ggcgtcctgc atcgccggcg ccgg gcc 117
 Ala
 1

aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165
 Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
 5 10 15

aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213
 Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
 20 25 30

gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261
 Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
 35 40 45

tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg 309
 Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu
 50 55 60 65

cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc 357
 Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys
 70 75 80

gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc 405
 Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly
 85 90 95

tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc 453
 Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg
 100 105 110

tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc 501
 Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro

115	120	125	
acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac			549
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn			
130	135	140	145
gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag			597
Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys			
	150	155	160
ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg			645
Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu			
	165	170	175
tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac			693
Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His			
	180	185	190
tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc			741
Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly			
	195	200	205
gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg			789
Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val			
	210	215	225
gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac			837
Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His			
	230	235	240
gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac			885
Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His			
	245	250	255
gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg			933
Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu			
	260	265	270
gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac			981
Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp			
	275	280	285
cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg			1029
Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu			
	290	295	300
atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc			1077
Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro			
	310	315	320
aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag			1125
Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys			
	325	330	335
gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc			1173
Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg			
	340	345	350
ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc			1221
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala			
	355	360	365

acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag 1269
 Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu
 370 375 380 385

tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg 1317
 Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu
 390 395 400

cgg gcc cct ttc cct tga taa 1338
 Arg Ala Pro Phe Pro
 405

<210> 3
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 3
 agctggctag ccactgggca ggtaagtatc a 31

<210> 4
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 4
 tggcgggatc cttaagagct gtaattgaac t 31

<210> 5
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
 tcagctcgag agcggtagcg ccc 23

<210> 6
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
 cccattctag aaaagcggaa cgccagcaaa ccccaggg 28

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
gctgagcggg ccaaacttt ttggattagc 30

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
gctaatacaa aagtgtttgg tccgctcagc 30

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
ccaaactggt ttggcgcagc tatagcgatg 30

<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
catcgctata gctgcgcaa aacagtttgg 30

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
aactgttttg gattcagtat agcgatggcg 30

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
cgccatcgct atactgaatc caaaacagtt 30

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
aacgggggct cctgcgagga ccagctgcag 30

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
ctgcagctgg tcctcgagga agccccggt 30

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
gggggctcct gccgcgacca gctgcagagc 30

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
gctctgcagc tggtcgcggc aggagcccc 30

<210> 17

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
gagctatatc tgcgagtgcc tgcctgcctt

30

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
aaggcaggca ggcactcgca gatatagctc

30

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
ggggcgcaat tgccagaccc ataaggatga

30

<210> 20
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
tcataccttat gggctctggcaa ttgcgcccc

30

<210> 21
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
gagcggacca aagagtttttg attagc

26

<210> 22
<211> 26

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
gctaataccaa aactcttttggg ccgctg 26

<210> 23
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
gagcggacca aacagttttgg attagc 26

<210> 24
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
gctaataccaa aactgttttggg ccgctc 26

<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
ctgcaaagac cagcagcagag ctatatctgc 30

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gcagatatag ctctgctgctg gtctttgcag 30

<210> 27
<211> 30
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 27
ctgcaaagac cagtcccagag ctatatctgc 30

<210> 28
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 28
gcagatatag ctctgggactg gtctttgcag 30

<210> 29
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29
cagagctata tctgcgactgc ctgcctgcc 29

<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30
ggcaggcagg cagtcgcagat atagctctg 29

<210> 31
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 31
cagagctata tctgctactgc ctgcctgc 28

<210> 32
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 32

gcaggcaggc agtagcagata tagctctg

28

<210> 33

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 33

gaacgggggc tcctgcgagga ccagcagcag agctatatct gc

42

<210> 34

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 34

gcagatatag ctctgctgctg gtcctcgcag gagcccccg t c

42